CLAIMS

1. A mass analysis method whereby a sample is ionized and a protein is analyzed using a mass analysis apparatus, said method comprising:

selecting predetermined information from a database in which information about proteins and peptides is stored, estimating the mass of the selected component, and calculating frequency information for each mass; and

analyzing a sample using a mass analysis apparatus so as to acquire a mass spectrum, selecting, based on the acquired mass spectrum and said frequency information, a mass to be used for identification, performing mass analysis using the mass spectrum of the selected mass as a precursor ion, and performing an identification process using a resultant mass spectrum.

2. The mass analysis method according to claim 1, further comprising, when the mass of the component information obtained from said database is estimated, estimating a peptide that will be obtained by enzymatically digesting each protein with a predetermined digestive enzyme, and estimating the mass of each peptide.

3. The mass analysis method according to claim 1, further comprising pre-setting the number of said precursor ions that are selected.

4. A mass analysis method whereby a sample is ionized and a protein is analyzed using a mass analysis apparatus, comprising the steps of:

(A) obtaining information about a plurality of proteins from an external database in which information about proteins is stored;

(B) estimating the mass of each of said obtained proteins;

(C) calculating a weight pattern by conducting normalization such that 1 is given when there is said estimated mass and 0 is given when there is no

such estimated mass, summing the estimation results for all of the proteins so as to determine a frequency for each mass;

(D) measuring a sample and acquiring a mass spectrum;

(E) normalizing the spectrum of the sample such that 1 is given when there is a mass and 0 is given when there is no mass;

(F) creating a pseudospectrum by superposing said spectrum of an actual sample that has been normalized on said weight pattern; and

(G) selecting a precursor ion to be subjected to MS/MS analysis from said mass spectrum of said sample based on the created pseudospectrum.

5. The mass analysis method according to claim 4, further comprising creating, when said weight pattern is calculated, a first pattern for weighting in order of decreasing frequency and a second pattern for weighting in order of increasing frequency.

6. The mass analysis method according to claim 5, wherein the mass for which the weighting value indicates the highest value in said second pattern is eliminated when the precursor ion to be subjected to MS/MS analysis is selected.

7. The mass analysis method according to claim 4, wherein a plurality of conditions are set when information is obtained from said database, and said steps (B) and (C) are performed for each item of information obtained in accordance with each of said set conditions, and the difference in frequency of the weight patterns according to each of said set conditions is determined so as to obtain a new weight pattern.

8. A mass analysis apparatus comprising:

an ionization unit for ionizing a sample;

a mass analysis unit for performing mass analysis; and

a data processing unit for setting analysis conditions and performing data processing on an analysis result,

wherein said data processing unit performs:

a preparation process in which information is obtained in accordance with a preset condition from a database in which information about proteins is stored, and the number of masses for which peaks associated with the obtained proteins exist are counted and rendered into frequency information; and

a precursor ion selection process in which precursor ions to be subjected to MS/MS analysis are selected in light of a mass spectrum obtained by subjecting an actual sample to mass analysis and in accordance with the frequency based on said frequency information.

9. The mass analysis apparatus according to claim 8, wherein said data processing unit comprises a display unit, wherein said display unit displays said frequency information for each of the masses, wherein said mass spectrum obtained by mass analysis of said actual sample is superposed on the displayed contents.

10. The mass analysis apparatus according to claim 8, wherein whether or not each of the peaks in said mass spectrum obtained by mass analysis of said actual sample has been selected as a precursor ion is displayed.